

Serial Number: 09/229,751A

ENTERED

H29

Changed a file from non-ASCII to ASCII

Changed the margins in cases where the sequence text was "wrapped" down to the next line.

Edited a format error in the Current Application Data section, specifically: #12

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other _____

Added the mandatory heading and subheadings for "Current Application Data".

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

Changed the spelling of a mandatory field (the headings or subheadings), specifically:

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

79

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

Inserted colons after headings/subheadings. Headings edited included:

RECEIVED

DEC 11 2000

Deleted extra, invalid, headings used by an applicant, specifically:

Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file;
 page numbers throughout text; other invalid text, such as _____

Inserted mandatory headings, specifically: _____

Corrected an obvious error in the response, specifically:

Edited identifiers where upper case is used but lower case is required, or vice versa.

Corrected an error in the Number of Sequences field, specifically:

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____Other:

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING DATE: 11/27/2000
PATENT APPLICATION: US/09/229,751A TIME: 17:42:32

Input Set : A:\PTO.txt
Output Set: N:\CRF3\11272000\I229751A.raw

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

ERRORRED SEQUENCES

- 64 (2) INFORMATION FOR SEQ ID NO: 2:
66 (i) SEQUENCE CHARACTERISTICS:
67 (A) LENGTH: 21 base pairs
68 (B) TYPE: nucleic acid
69 (C) STRANDEDNESS: single
70 (D) TOPOLOGY: unknown
72 (ii) MOLECULE TYPE: DNA (genomic)
74 (iii) HYPOTHETICAL: NO
76 (iv) ANTI-SENSE: NO
80 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
E--> 82 AATCATTTT TGATTAAGCC G
W--> 83 21
85 (2) INFORMATION FOR SEQ ID NO: 3:

RAW SEQUENCE LISTING
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87      (i) SEQUENCE CHARACTERISTICS:
88          (A) LENGTH: 21 base pairs
89          (B) TYPE: nucleic acid
90          (C) STRANDEDNESS: single
91          (D) TOPOLOGY: unknown
93      (ii) MOLECULE TYPE: DNA (genomic)
95      (iii) HYPOTHETICAL: NO
97      (iv) ANTI-SENSE: NO
101     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
E--> 103 AATCATTTC TGAGGTCTCC G
W--> 104   21
127 (2) INFORMATION FOR SEQ ID NO: 5:
129      (i) SEQUENCE CHARACTERISTICS:
130          (A) LENGTH: 21 base pairs
131          (B) TYPE: nucleic acid
132          (C) STRANDEDNESS: single
133          (D) TOPOLOGY: unknown
135      (ii) MOLECULE TYPE: DNA (genomic)
137      (iii) HYPOTHETICAL: NO
139      (iv) ANTI-SENSE: NO
143     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
E--> 145 AATCATTTTC TTCCTAAAGGT G
W--> 146   21
148 (2) INFORMATION FOR SEQ ID NO: 6:
150      (i) SEQUENCE CHARACTERISTICS:
151          (A) LENGTH: 21 base pairs
152          (B) TYPE: nucleic acid
153          (C) STRANDEDNESS: single
154          (D) TOPOLOGY: unknown
156      (ii) MOLECULE TYPE: DNA (genomic)
158      (iii) HYPOTHETICAL: NO
160      (iv) ANTI-SENSE: NO
164     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
E--> 166 AATCATTTTC TGTTGCCGCC G
W--> 167   21
169 (2) INFORMATION FOR SEQ ID NO: 7:
171      (i) SEQUENCE CHARACTERISTICS:
172          (A) LENGTH: 21 base pairs
173          (B) TYPE: nucleic acid
174          (C) STRANDEDNESS: single
175          (D) TOPOLOGY: unknown
177      (ii) MOLECULE TYPE: peptide
179      (iii) HYPOTHETICAL: NO
181      (iv) ANTI-SENSE: NO
185     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
E--> 187 AATCATTTTC TGCCTCGTTG G
W--> 188   21
190 (2) INFORMATION FOR SEQ ID NO: 8:
192     (i) SEQUENCE CHARACTERISTICS:

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same
error

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Input Set : A:\PTO.txt
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193 (A) LENGTH: 21 base pairs
194 (B) TYPE: nucleic acid
195 (C) STRANDEDNESS: single
196 (D) TOPOLOGY: unknown
198 (ii) MOLECULE TYPE: peptide
200 (iii) HYPOTHETICAL: NO
202 (iv) ANTI-SENSE: NO
206 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
E--> 208 AATCATTTT TGCCCTCTCG G
W--> 209 21
211 (2) INFORMATION FOR SEQ ID NO: 9:
213 (i) SEQUENCE CHARACTERISTICS:
214 (A) LENGTH: 21 base pairs
215 (B) TYPE: nucleic acid
216 (C) STRANDEDNESS: single
217 (D) TOPOLOGY: unknown
219 (ii) MOLECULE TYPE: DNA (genomic)
221 (iii) HYPOTHETICAL: NO
223 (iv) ANTI-SENSE: NO
227 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
E--> 229 AATCATTTC TGATGCCGAA G
W--> 230 21
232 (2) INFORMATION FOR SEQ ID NO: 10:
234 (i) SEQUENCE CHARACTERISTICS:
235 (A) LENGTH: 21 base pairs
236 (B) TYPE: nucleic acid
237 (C) STRANDEDNESS: single
238 (D) TOPOLOGY: unknown
240 (ii) MOLECULE TYPE: DNA (genomic)
242 (iii) HYPOTHETICAL: NO
244 (iv) ANTI-SENSE: NO
248 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
E--> 250 AATCATTTC TGCCTACTGG G
W--> 251 21
253 (2) INFORMATION FOR SEQ ID NO: 11:
255 (i) SEQUENCE CHARACTERISTICS:
256 (A) LENGTH: 21 base pairs
257 (B) TYPE: nucleic acid
258 (C) STRANDEDNESS: single
259 (D) TOPOLOGY: unknown
261 (ii) MOLECULE TYPE: DNA (genomic)
263 (iii) HYPOTHETICAL: NO
265 (iv) ANTI-SENSE: NO
269 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
E--> 271 AATCATTTC TTAAGGGGAC G
W--> 272 21
274 (2) INFORMATION FOR SEQ ID NO: 12:
276 (i) SEQUENCE CHARACTERISTICS:
277 (A) LENGTH: 21 base pairs

same

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Input Set : A:\PTO.txt
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278 (B) TYPE: nucleic acid
279 (C) STRANDEDNESS: single
280 (D) TOPOLOGY: unknown
282 (ii) MOLECULE TYPE: DNA (genomic)
284 (iii) HYPOTHETICAL: NO
286 (iv) ANTI-SENSE: NO
290 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
E--> 292 ATTCAATTTC TTCTTTGGCG T
W--> 293 21
295 (2) INFORMATION FOR SEQ ID NO: 13:
297 (i) SEQUENCE CHARACTERISTICS:
298 (A) LENGTH: 21 base pairs
299 (B) TYPE: nucleic acid
300 (C) STRANDEDNESS: single
301 (D) TOPOLOGY: unknown
303 (ii) MOLECULE TYPE: DNA (genomic)
305 (iii) HYPOTHETICAL: NO
307 (iv) ANTI-SENSE: NO
311 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
E--> 313 AATCAATTTC TGATTAGGAA G
W--> 314 21
316 (2) INFORMATION FOR SEQ ID NO: 14:
318 (i) SEQUENCE CHARACTERISTICS:
319 (A) LENGTH: 21 base pairs
320 (B) TYPE: nucleic acid
321 (C) STRANDEDNESS: single
322 (D) TOPOLOGY: unknown
324 (ii) MOLECULE TYPE: DNA (genomic)
326 (iii) HYPOTHETICAL: NO
328 (iv) ANTI-SENSE: NO
332 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
E--> 334 AATCAATTTC TGCCGACTGC T
W--> 335 21
379 (2) INFORMATION FOR SEQ ID NO: 17:
381 (i) SEQUENCE CHARACTERISTICS:
382 (A) LENGTH: 21 base pairs
383 (B) TYPE: nucleic acid
384 (C) STRANDEDNESS: single
385 (D) TOPOLOGY: unknown
387 (ii) MOLECULE TYPE: DNA (genomic)
389 (iii) HYPOTHETICAL: NO
391 (iv) ANTI-SENSE: NO
395 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
E--> 397 ATTCAATTTC TGCCGCAGAA T
W--> 398 21
989 (2) INFORMATION FOR SEQ ID NO: 46:
991 (i) SEQUENCE CHARACTERISTICS:
992 (A) LENGTH: 21 base pairs
993 (B) TYPE: nucleic acid



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994      (C) STRANDEDNESS: single
995      (D) TOPOLOGY: unknown
997      (ii) MOLECULE TYPE: DNA (genomic)
999      (iii) HYPOTHETICAL: NO
1001      (iv) ANTI-SENSE: NO
1005      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:
E--> 1007 ACGCATCGTT TGCCTTCTCG G
W--> 1008 21
1010 (2) INFORMATION FOR SEQ ID NO: 47:
1012      (i) SEQUENCE CHARACTERISTICS:
1013          (A) LENGTH: 21 base pairs
1014          (B) TYPE: nucleic acid
1015          (C) STRANDEDNESS: single
1016          (D) TOPOLOGY: unknown
1018      (ii) MOLECULE TYPE: DNA (genomic)
1020      (iii) HYPOTHETICAL: NO
1022      (iv) ANTI-SENSE: NO
1026      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:
E--> 1028 GTTACTAGTA GGGGAAATGT T
W--> 1029 21
1031 (2) INFORMATION FOR SEQ ID NO: 48:
1033      (i) SEQUENCE CHARACTERISTICS:
1034          (A) LENGTH: 21 base pairs
1035          (B) TYPE: nucleic acid
1036          (C) STRANDEDNESS: single
1037          (D) TOPOLOGY: unknown
1039      (ii) MOLECULE TYPE: DNA (genomic)
1041      (iii) HYPOTHETICAL: NO
1043      (iv) ANTI-SENSE: NO
1047      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:
E--> 1049 AAGCTGTGGG TGATTCCTCA G
W--> 1050 21
1052 (2) INFORMATION FOR SEQ ID NO: 49:
1054      (i) SEQUENCE CHARACTERISTICS:
1055          (A) LENGTH: 21 base pairs
1056          (B) TYPE: nucleic acid
1057          (C) STRANDEDNESS: single
1058          (D) TOPOLOGY: unknown
1060      (ii) MOLECULE TYPE: DNA (genomic)
1062      (iii) HYPOTHETICAL: NO
1064      (iv) ANTI-SENSE: NO
1068      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:
E--> 1070 TATTCGCCCTC CTCATAGGCA T
W--> 1071 21
1220 (2) INFORMATION FOR SEQ ID NO: 57:
1222      (i) SEQUENCE CHARACTERISTICS:
1223          (A) LENGTH: 21 base pairs
1224          (B) TYPE: nucleic acid
1225          (C) STRANDEDNESS: single

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1226      (D) TOPOLOGY: unknown
1228      (ii) MOLECULE TYPE: DNA (genomic)
1230      (iii) HYPOTHETICAL: NO
1232      (iv) ANTI-SENSE: NO
1236      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:
E--> 1238 TCGTATCCTC CGTATTTGA T
W--> 1239      21
1241 (2) INFORMATION FOR SEQ ID NO: 58:
1243      (i) SEQUENCE CHARACTERISTICS:
1244          (A) LENGTH: 21 base pairs
1245          (B) TYPE: nucleic acid
1246          (C) STRANDEDNESS: single
1247          (D) TOPOLOGY: unknown
1249      (ii) MOLECULE TYPE: DNA (genomic)
1251      (iii) HYPOTHETICAL: NO
1253      (iv) ANTI-SENSE: NO
1257      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:
E--> 1259 CTTTTGTCGC CTCTGCATCG T
W--> 1260      21
1262 (2) INFORMATION FOR SEQ ID NO: 59:
1264      (i) SEQUENCE CHARACTERISTICS:
1265          (A) LENGTH: 21 base pairs
1266          (B) TYPE: nucleic acid
1267          (C) STRANDEDNESS: single
1268          (D) TOPOLOGY: unknown
1270      (ii) MOLECULE TYPE: DNA (genomic)
1272      (iii) HYPOTHETICAL: NO
1274      (iv) ANTI-SENSE: NO
1278      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:
E--> 1280 TTTGATTCCTC CGCTTCGTCG G
W--> 1281      21
1662 (2) INFORMATION FOR SEQ ID NO: 78:
1664      (i) SEQUENCE CHARACTERISTICS:
1665          (A) LENGTH: 7 amino acids
1666          (B) TYPE: amino acid
1667          (C) STRANDEDNESS: single
1668          (D) TOPOLOGY: unknown
1670      (ii) MOLECULE TYPE: peptide
1672      (iii) HYPOTHETICAL: NO
1674      (iv) ANTI-SENSE: NO
1678      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:
1680      Phe Asp Ser Pro Leu Arg Arg
1681      1      5
1683 (2) INFORMATION FOR SEQ ID NO: 78:
1685      (i) SEQUENCE CHARACTERISTICS:
1686          (A) LENGTH: 7 amino acids
1687          (B) TYPE: amino acid
1688          (C) STRANDEDNESS: single
1689          (D) TOPOLOGY: unknown

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Same

RAW SEQUENCE LISTING DATE: 11/27/2000
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Input Set : A:\PTO.txt
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1691 (iii) MOLECULE TYPE: peptide
1693 (iii) HYPOTHETICAL: NO
1695 (iv) ANTI-SENSE: NO
E--> 1699 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79
1701 Trp Ser Pro Leu His Lys His
1702 1 5
E--> 1704 (2) INFORMATION FOR SEQ ID NO: 80:
1706 (i) SEQUENCE CHARACTERISTICS:
1707 (A) LENGTH: 12 amino acids
1708 (B) TYPE: amino acid
1709 (C) STRANDEDNESS: single
1710 (D) TOPOLOGY: unknown
1712 (ii) MOLECULE TYPE: peptide
1714 (iii) HYPOTHETICAL: NO
1715 (iv) ANTI-SENSE: NO
1720 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:
1722 Asn His Phe Leu Lys Ser Gln Pro Gly Val Val Thr
1723 1 5 10

OK

VERIFICATION SUMMARY DATE: 11/27/2000
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Input Set : A:\PTO.txt
Output Set: N:\CRF3\11272000\I229751A.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:82 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:2
L:83 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:103 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:3
L:104 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:145 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:5
L:146 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:166 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:6
L:167 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:187 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:7
L:188 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:208 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:8
L:209 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:229 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:9
L:230 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:250 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:10
L:251 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:271 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:11
L:272 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:292 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:12
L:293 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:313 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:13
L:314 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:334 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:14
L:335 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:397 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:17
L:398 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:1007 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:46
L:1008 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:46
L:1028 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:47
L:1029 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:47
L:1049 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:48
L:1050 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:48
L:1070 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:49
L:1071 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:49
L:1238 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:57
L:1239 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:57
L:1259 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:58
L:1260 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:58
L:1280 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:59
L:1281 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:59
L:1301 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:60
L:1302 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:60
L:1322 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:61
L:1323 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:61
L:1343 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:62
L:1344 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:62

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Input Set : A:\PTO.txt
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L:1364 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:63
L:1365 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:63
L:1385 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:64
L:1386 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:64
L:1406 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:65
L:1407 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:65
L:1427 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:66
L:1428 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:66
L:1449 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:67
L:1450 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:67
L:1470 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:68
L:1471 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:68
L:1491 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:69
L:1492 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:69
L:1512 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:70
L:1513 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:70
L:1533 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:71
L:1534 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:71
L:1699 M:212 E: (34) Invalid or duplicate Sequence ID Number, Data=[79:]
L:1704 M:216 E: (34) Seq.#s missing, 81 thru 79